icon96™

Amplify. Quantify. Normalize. **All at Once.**

The world's first thermocycler with 96
individually controlled wells and built-in AutoNorm™

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Normalized, sequencing-ready libraries **in one step**

The best possible data from every sample with iconPCR™ and AutoNorm

- icon96 delivers sequencing-ready libraries in one step—powered by iconPCR technology with AutoNorm
- Automates the most labor-intensive, error-prone part of NGS library prep
- No more manual quantification, normalization, or guesswork
- Every sample, no matter the input or quality, is normalized automatically for consistent, high-quality sequencing

Workflow Improvements:

- The end of manual normalization
- Eliminates need for quantification, dilution, or normalization consumables
- Up to 60% less hands-on time

Data Quality:

- Boost sequencing throughput
- Reject fewer samples
- Reliable results from a wider range of inputs
- Significantly reduced artifacts and amplification bias

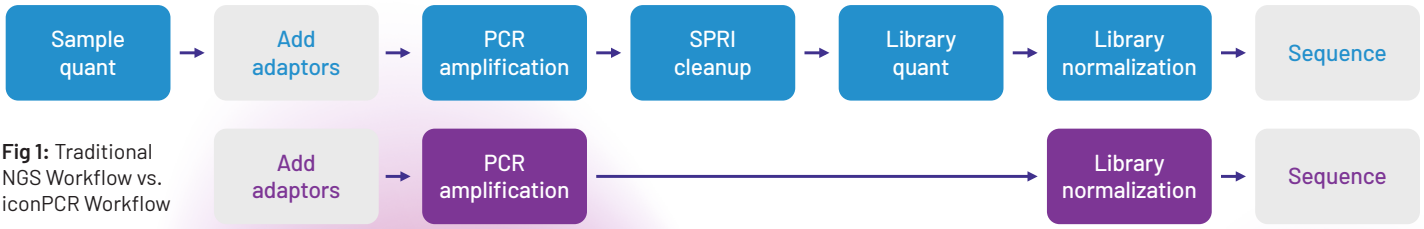

Fig 1: Traditional NGS Workflow vs. iconPCR Workflow

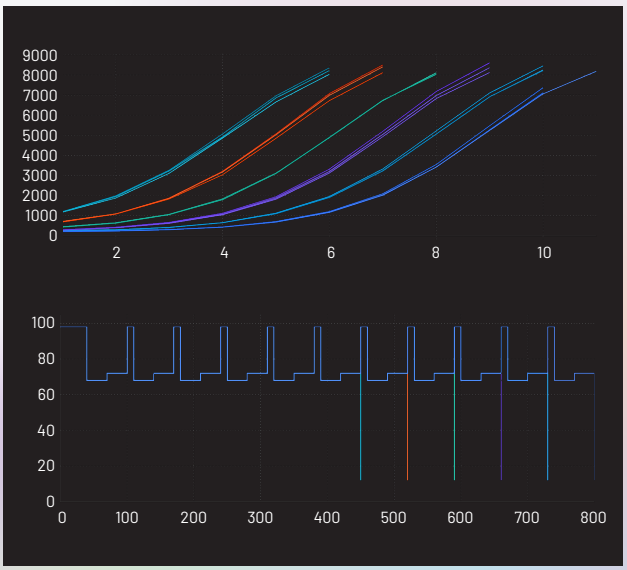

Fig 2: AutoNorm simplifies workflows and improves data quality. Users set a target amplification level, and each well stops cycling automatically once that level is reached. Shown is a dilution series of DNA libraries with fluorescence (top) and individual well temperatures (bottom) tracked in real time. High-concentration samples (light blue) reach the threshold first and enter a cold-hold phase, while lower-concentration wells continue cycling. Each sample stops precisely at the optimal point, with no manual intervention required.

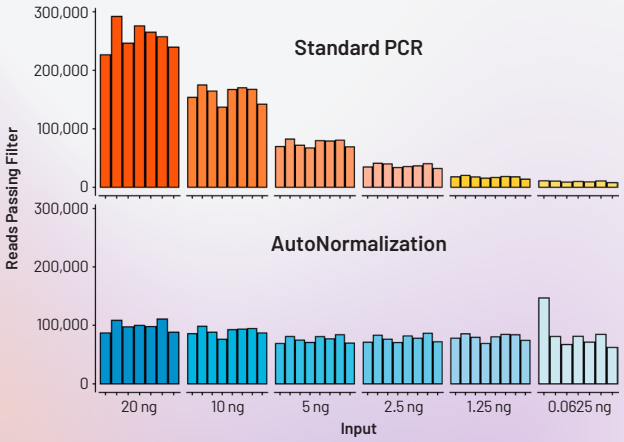

Fig 3: Here we show the significant yield variance when using a single PCR instrument with a fixed number of PCR cycles compared to iconPCR with AutoNorm where each sample is amplified to similar levels.

Shorter workflows, lower costs, and higher quality data

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Real-World Impact: Application Spotlights

Metagenomics

Why iconPCR?

Standard methods create errors, bias, and wasted time.

How it Works:

The iconPCR method auto-normalizes diverse samples, reduces chimeras, and streamlines pooling.

- 46% fewer chimeras in 16S libraries
- 2x increase in Shannon Diversity Index
- Over $15,000 saved in a 1,000-sample study

> **Support hundreds of diverse projects each month with 50% less hands-on time.**

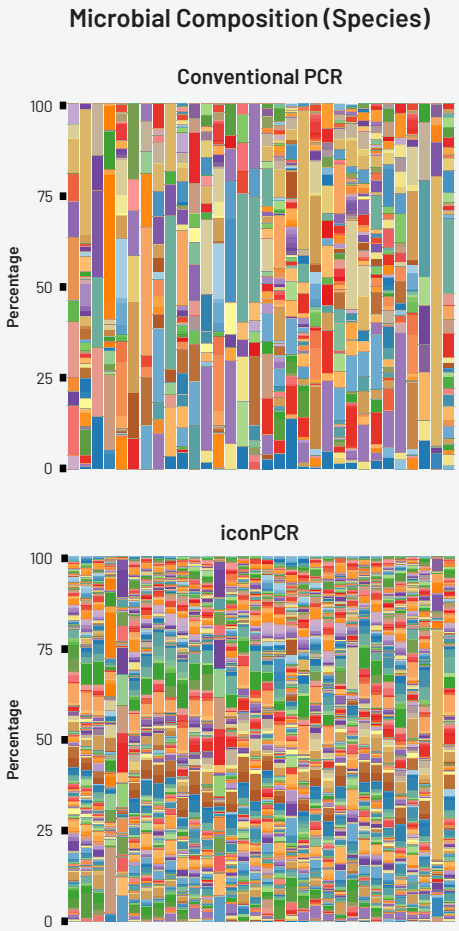

Fig. 4: Soil metagenomic samples using 1500 bp v9 16S amplicons sequenced using long read technology. Each color represents an independent species. icon96-generated libraries represent a much more accurate level of diversity by limiting the required amplification and prohibiting the over-amplification of high abundance species.

WGS (incl. degraded/FFPE samples)

Why iconPCR?

Whole genome sequencing demands efficiency and consistency, even with variable sample quality. Traditional workflows require multiple PCR runs and manual quantification, often yielding inconsistent results. iconPCR with AutoNorm eliminates these hurdles: each sample—regardless of DNA quantity or integrity, including FFPE—automatically reaches optimal amplification. The result: balanced, normalized libraries ready for pooling in a single run.

How it Works:

AutoNorm makes balancing and normalization automatic, fast, and reliable for every sample—no matter the input.

- Individual real-time amplification for each genome
- Automatic normalization—no manual quant or adjustment needed
- Prevents over/under-amplification, even for FFPE and low-input DNA
- Balanced libraries—direct-to-pool for seamless sequencing

> **Run diverse genomes together, amplify once, pool with precision—discover truly balanced sequencing at scale.**

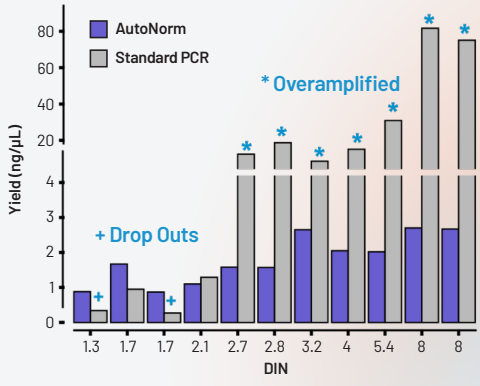

Fig 5: AutoNorm delivers consistent library yields from FFPE samples, independent of DNA quality. Standard PCR produced variable yields—high for intact DNA, low for degraded. AutoNorm enabled uniform amplification across all samples, preventing over- or under-amplification and streamlining NGS library prep from FFPE inputs.

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Single-Cell RNA-Seq

Why iconPCR?

iconPCR with AutoNorm removes the need for workflow splitting and manual calibration in single cell RNA-seq, delivering optimal amplification and streamlined processing, regardless of cell number or sample complexity.

How it Works:

iconPCR automates single cell workflows by controlling PCR cycling in real time for each well.

- Real-time per-well fluorescence monitoring precisely stops amplification at the ideal endpoint for each sample, regardless of input amount or cell type
- Eliminates cycle adjustments and separate PCR runs across different cell types or inputs—process all samples together in one run
- Delivers uniform, balanced libraries automatically, minimizing manual intervention and hands-on time
- Maintains robust data quality and biological accuracy, matching conventional results for gene and UMI detection

icon96 simplifies single cell workflows while maintaining unbeatable RNA-seq data quality, enabling higher throughput with fewer errors.

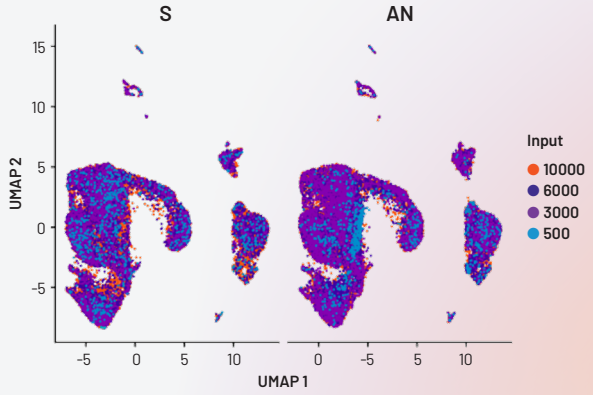

Fig. 6: Clustering of all samples reveals common gene signatures. Clustering of all samples revealed no differences between the standard PCR method and AutoNorm, showcasing that the change in workflow does not alter data quality.

RNA-Sequencing

Why iconPCR?

iconPCR with AutoNorm streamlines RNA-seq library prep by removing individual purification and quantification steps. Every sample—regardless of input quality or RNA integrity—receives precisely optimized amplification for reliable, high-quality results, even from FFPE or degraded inputs.

How it Works:

iconPCR ensures uniform outcomes and reproducibility across all RNA-seq samples.

- Real-time, well-specific feedback stops PCR at the optimal point for each sample.
- No manual input quantification or workflow splitting required.
- Prevents under- and over-amplification, including for challenging samples like FFPE or degraded RNA.
- Enables simultaneous processing of mixed-quality samples with up to 50% less hands-on time.
- Delivers higher gene detection rates, reduced PCR artifacts, and consistent, high-quality data.

Confidently generate robust, reproducible RNA-seq libraries across all sample types—without added complexity.

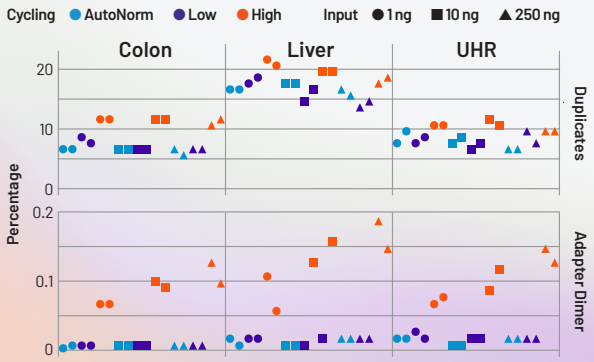

Fig. 7: AutoNorm prevents overamplification artifacts. Overcycled libraries (orange) showed higher levels of adapter dimers and PCR duplicates than libraries amplified with either a low fixed-cycle protocol (dark blue) or AutoNorm (light blue). These trends were consistent across input amounts (circles, 1 ng; squares, 10 ng; triangles, 250 ng).

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